

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=16; hr=8; min=55; sec=13; ms=601;]

=====

Application No: 10597719 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-08-14 12:29:23.193
Finished: 2008-08-14 12:29:24.744
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 551 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

SEQUENCE LISTING

<110> Syngenta Ltd

<120> Methods for screening insecticides

<130> PPD 50397/WO

<140> 10597719

<141> 2008-08-14

<160> 21

<170> PatentIn version 3.1

<210> 1

<211> 2797

<212> DNA

<213> D. melanogaster

<400> 1

gttcattaaa atatgtggtg ataacgcgag ctgccgaatc tgcgtgcaat tcgtgcgttt	60
gacgtgggta ctaactgcta tgctgtcgcg cggacagttg ttctgatacg cagagttcct	120
gcctcaccac acacgaccac ctccattaaa accagccacc cccccagcg cctcctccac	180
cgacagcagc tgctccaccg caccaccagg agagggggcaa ttaaaaaatc aatcagaggg	240
ccctaattga aagctgccac cgtcgaaatg tcgccgccga agaactgcgc ggtgtgcggg	300
gacaaggctc tgggctacaa cttcaatgcg gtcacctgcg agagctgcaa ggcgttcttc	360
cgacggaacg cgctggccaa gaagcagttc acctgccctt tcaaccaaaa ctgcgacatc	420
actgtggtca ctcgacgctt ctgccagaaa tgccgcctgc gcaagtgcct ggatatcggg	480
atgaagagtg aaaacattat gtccgaggag gacaagctga tcaagcggcg caagatcgag	540
accaaccggg ccaagcgacg cctcatggag aacggcacgg atgcgtgcga cgccgatggc	600

ggcgaggaaa	gggatcacaa	agcgccggcg	gatagcagca	gcagcaacct	tgaccactac	660
tcgggggtcac	aggactcgca	gagctgcggc	tcggcggaca	gcgggggcaa	tgggtgctcc	720
ggcagacagg	ccagttcgcc	gggcacacag	gtcaatccgc	ttcagatgac	ggccgagaag	780
atagtcgacc	agatcgtatc	cgacccggat	cgagcctcgc	aggccatcaa	ccggttgatg	840
cgcacgcaga	aagaggctat	atcggtgatg	gagaaggtaa	tcagctcaca	aaaggacgcc	900
ttaaggctgg	tgtcgcatTT	gatcgactat	ccaggcgacg	cactcaagat	catttcaaag	960
tttatgaact	cgccctttaa	cgcgctgaca	gtattcacca	aattcatgag	ctcaccacg	1020
gacggcgttg	aaattatctc	aaagatagtt	gattcgcccc	cggacgtgg	ggagttcatg	1080
cagaacttga	tgcactcgcc	agaggacgcc	atcgatataa	tgaacaagtt	catgaatacc	1140
ccagcggagg	cgctgcgcat	tcttaaccga	atcctaagcg	gcggaggagc	gaacgcagcc	1200
cagcagacag	cagaccgcaa	gccattgctg	gacaaggagc	cggcggtgaa	gcctgcagcg	1260
ccagcggagc	gagctgatac	tgtcattcaa	agcatgctgg	gcaacagtcc	gccaatttcg	1320
ccacatgatg	ctgccgtgga	tctgcagtac	cactcgcccc	gtgtcgggga	gcagcccagt	1380
acatcgagta	gccaccctt	gccttacata	gccaaactcg	cggacttcga	tctgaagacc	1440
ttcatgcaga	ccaactacaa	cgacgagccc	agtctggaca	gtgattttag	cattaactca	1500
atcgaatcgg	tgctatccga	ggtgatccgc	attgagtacc	aggccttcaa	tagcatacaa	1560
caagcggcat	cgcgcgtaaa	ggaggagatg	tcctacggca	ctcagtctac	gtacggtgga	1620
tgcaattcgg	ctgcaaacaa	tagccagccg	cacctgcagc	aacccatctg	cgccccatcc	1680
accagcagt	tggatcgcg	gctaaacgag	gcggagcaaa	tgaagctgcg	ggagctgcga	1740
ctggccagcg	aggctcttta	tgatcccgtg	gacgaggacc	tcagcgccct	gatgatgggc	1800
gatgatcgca	ttaagcccga	cgacactcgc	cacaacccaa	agctattgca	gctgatcaat	1860
ctgacggcgg	tggccatcaa	gcggcttatc	aaaatggcca	agaagattac	agcattccgt	1920
gacatgtgcc	aggaggacca	ggtggcccta	ctcaaagggtg	gctgcacaga	aatgatgata	1980
atgcgctccg	taatgattta	cgacgacgat	cgcgccgcct	ggaaggtagc	ccataccaaa	2040
gagaacatgg	gcaacatacg	cactgacctg	ctcaagtttg	ccgaaggcaa	tatctacgag	2100
gagcaccaaa	agttcatcac	aacgtttgac	gagaagtggc	gcatggacga	gaacataatc	2160
ctgatcatgt	gtgccattgt	cctttttacc	tcggetcgat	cgcgagtgat	acacaaagac	2220
gtgattagat	tggaacagaa	ttcctactat	tatcttctgc	gaagatatct	ggagagtgtt	2280

tattctggct gtgaggcgag aaacgcgttt atcaagctaa tccaaaagat ttcagatgtg 2340
gagcgtctga acaagttcat aattaatgtc tatttgaatg ttaacccatc ccaggtggag 2400
cccttgctgc gtgaaatatt cgatttgaaa aatcactaga caaccgatgc gtgtcgggca 2460
tttaatgcct atgttgatgc ccaatgatga atggccaaca agctgtagtt gttgttgttg 2520
ttgatgtctg ttttatcttg tcgcttgtaa tgtagattt taatcgaatg tgattgtag 2580
atttgcatac actgcataga ttttatatct ctacatcaaa gagagcatat ttaggatacc 2640
aagtgcacag caacacaatc tatatgtaac gtacaccgtt tacctagttt caataaaact 2700
agacgataat gcaataacta acttggaagc gtgggttctg tgcaaaaagg aaaaaagaca 2760
aaaaaaataa actgactttg agaaccagtg gtaaacc 2797

<210> 2

<211> 36

<212> DNA

<213> Artificial sequence

<220>

<223> Primer dhr96-F

<400> 2

tattgcggat ccttgacgtg ggtactaact gctatg 36

<210> 3

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Primer dhr96-R

<400> 3

agtccggaat tcagtagtgg tcaaggttgc tgct 34

<210> 4

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> dhr96-fwd_primer

<400> 4

catggacgag aacataatcc tgat

24

<210> 5

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> dhr96-rev_primer

<400> 5

cagaagataa tagtaggaat tctgttccaa

30

<210> 6

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<223> dhr96-taqman_probe

<400> 6

tgtgccattg tcctttttac ctcggct

27

<210> 7

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> RpL32-fwd_primer

<400> 7

gatatgctaa gctgtcgcac aaat

24

<210> 8

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> RpL32-rev_primer

<400> 8

ggcatcagat actgtccctt gaa

23

<210> 9

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> RpL32-taqman_probe

<400> 9

cgcaagccca agggatcga caac

24

<210> 10

<211> 263

<212> PRT

<213> Artificial sequence

<220>

<223> DHR96_peptide2

<400> 10

Thr Asp Gly Val Glu Ile Ile Ser Lys Ile Val Asp Ser Pro Ala Asp
1 5 10 15

Val Val Glu Phe Met Gln Asn Leu Met His Ser Pro Glu Asp Ala Ile
20 25 30

Asp Ile Met Asn Lys Phe Met Asn Thr Pro Ala Glu Ala Leu Arg Ile
35 40 45

Leu Asn Arg Ile Leu Ser Gly Gly Gly Ala Asn Ala Ala Gln Gln Thr
50 55 60

Ala Asp Arg Lys Pro Leu Leu Asp Lys Glu Pro Ala Val Lys Pro Ala
65 70 75 80

Ala Pro Ala Glu Arg Ala Asp Thr Val Ile Gln Ser Met Leu Gly Asn
85 90 95

Ser Pro Pro Ile Ser Pro His Asp Ala Ala Val Asp Leu Gln Tyr His
100 105 110

Ser Pro Gly Val Gly Glu Gln Pro Ser Thr Ser Ser Ser His Pro Leu
115 120 125

Pro Tyr Ile Ala Asn Ser Pro Asp Phe Asp Leu Lys Thr Phe Met Gln
130 135 140

Thr Asn Tyr Asn Asp Glu Pro Ser Leu Asp Ser Asp Phe Ser Ile Asn
145 150 155 160

Ser Ile Glu Ser Val Leu Ser Glu Val Ile Arg Ile Glu Tyr Gln Ala
165 170 175

Phe Asn Ser Ile Gln Gln Ala Ala Ser Arg Val Lys Glu Glu Met Ser
180 185 190

Tyr Gly Thr Gln Ser Thr Tyr Gly Gly Cys Asn Ser Ala Ala Asn Asn

195 200 205

Ser Gln Pro His Leu Gln Gln Pro Ile Cys Ala Pro Ser Thr Gln Gln
210 215 220

Leu Asp Arg Glu Leu Asn Glu Ala Glu Gln Met Lys Leu Arg Glu Leu
225 230 235 240

Arg Leu Ala Ser Glu Ala Leu Tyr Asp Pro Val Asp Glu Asp Leu Ser
245 250 255

Ala Leu Met Met Gly Asp Asp
260

<210> 11

<211> 440

<212> DNA

<213> D. melanogaster

<400> 11
atcccaaaac aaactgggta ttgtggtagg tcatttggtt ggcagaaaga aaactcgaga 60

aattttctctg gccggttatc gttattctct cttttctttt tgggtctctc cctctctgca 120

ctaattgctct ctactctgt cacacagtaa acggcatact gctctcggtg gttcgagaga 180

gcgcgcctcg aatgttcgcg aaaagagcgc cggagtataa atagaggcgc ttcgtctacg 240

gagcgacaat tcaattcaaa caagcaaagt gaacacgtcg ctaagcgaaa gctaagcaaa 300

taaacaagcg cagctgaaca agctaaacaa tctgcagtaa agtgcaagtt aaagtgaatc 360

aattaaaagt aaccagcaac caagtaaatc aactgcaact actgaaatct gccagaagt 420

aattattgaa tacaagaaga 440

<210> 12

<211> 441

<212> DNA

<213> S. cerevisiae

<400> 12
atgaagctac tgtcttctat cgaacaagca tgcgatattt gccgacttaa aaagctcaag 60

tgctccaaag aaaaaccgaa gtgcgccaag tgtctgaaga acaactggga gtgtcgctac 120

tctcccaaaa ccaaaaggct tccgctgact agggcacatc tgacagaagt ggaatcaagg 180

ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240

ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggattatt tgtacaagat 300

aatgtgaata aagatgccgt cacagataga ttggcttcag tggagactga tatgcctcta 360

acattgagac agcatagaat aagtgcgaca tcatcatcgg aagagagtag taacaaaggt 420

caaagacagt tgactgtatc g 441

<210> 13

<211> 147

<212> PRT

<213> S. cerevisiae

<400> 13

Met	Lys	Leu	Leu	Ser	Ser	Ile	Glu	Gln	Ala	Cys	Asp	Ile	Cys	Arg	Leu
1				5					10					15	
Lys	Lys	Leu	Lys	Cys	Ser	Lys	Glu	Lys	Pro	Lys	Cys	Ala	Lys	Cys	Leu
			20					25					30		
Lys	Asn	Asn	Trp	Glu	Cys	Arg	Tyr	Ser	Pro	Lys	Thr	Lys	Arg	Ser	Pro
		35					40					45			
Leu	Thr	Arg	Ala	His	Leu	Thr	Glu	Val	Glu	Ser	Arg	Leu	Glu	Arg	Leu
	50					55					60				
Glu	Gln	Leu	Phe	Leu	Leu	Ile	Phe	Pro	Arg	Glu	Asp	Leu	Asp	Met	Ile
65					70					75				80	
Leu	Lys	Met	Asp	Ser	Leu	Gln	Asp	Ile	Lys	Ala	Leu	Leu	Thr	Gly	Leu
				85					90					95	
Phe	Val	Gln	Asp	Asn	Val	Asn	Lys	Asp	Ala	Val	Thr	Asp	Arg	Leu	Ala
				100				105						110	

Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
130 135 140

Thr Val Ser
145

<210> 14

<211> 1944

<212> DNA

<213> D. melanogaster

<400> 14

aacattatgt ccgaggagga caagctgata aagcggcgca agatcgagac caaccgggcc	60
aagcgacgcc tcatggagaa cggcacggat gcgtgcgacg ccgatggcgg cgaggaaagg	120
gatcaciaaag cgccggcgga tagcagcagc agcaaccttg accactactc ggggtcacag	180
gactcgcaga gctgcggctc ggcggacagc gggggccaatg ggtgctccgg cagacaggcc	240
agttcgccgg gcacacaggt caatccgctt cagatgacgg ccgagaagat agtcgaccag	300
atcgtatccg acccggatcg agcctcgcag gccatcaacc ggttgatgcg cacgcagaaa	360
gaggctatat cggatgatga gaaggtaatc agctcaciaa aggacgcctt aaggctggtg	420
tcgcatttga tcgactatcc aggcgacgca ctcaagatca tttcaaagtt tatgaactcg	480
ccctttaacg cgctgacagt attcaccaaa ttcatagact caccacgga cggcgttgaa	540
attatctcaa agatagttga ttcgcccgcg gacgtggtgg agttcatgca gaacttgatg	600
cactcgccag aggacgccat cgatataatg aacaagttca tgaatacccc agcggaggcg	660
ctgcgcattc ttaaccgaat cctaagcggc ggaggagcga acgcagccca gcagacagca	720
gaccgcaagc cattgctgga caaggagccg gcggtgaagc ctgcagcgcc agcggagcga	780
gctgatactg tcattcaaag catgctgggc aacagtccgc caatttcgcc acatgatgct	840
gccgtggatc tgcagtagca ctgcgccggt gtcggggagc agcccagtag atcgagtagc	900
cacccttgc cttacatagc caactcgccg gacttcgata tgaagacctt catgcagacc	960
aactacaacg acgagcccag tctggacagt gattttagca ttaactcaat cgaatcgggtg	1020

ctatccgagg tgatccgcat tgagtaccag gccttcaata gcatacaaca agcggcatcg 1080
cgcgtaaagg aggagatgtc ctacggcact cagtctacgt acggtggatg caattcggct 1140
gcaaacaata gccagccgca cctgcagcaa cccatctgcg cccateccac ccagcagttg 1200
gatcgcgagc taaacgaggc ggagcaaatg aagctgcggg agctgcgact ggccagcgag 1260
gctctttatg atcccgtgga cgaggacctc agcgccctga tgatgggcga tgatcgcat 1320
aagcccgacg acactcgcca caacccaaag ctattgcagc tgatcaatct gacggcggtg 1380
gccatcaagc ggcttatcaa aatggccaag aagattacag cattccgtga catgtgccag 1440
gaggaccagg tggccctact caaaggtggc tgcacagaaa tgatgataat gcgctccgta 1500
atgatttacg acgacgatcg cgccgcctgg aaggtacccc ataccaaaga gaacatgggc 1560
aacatacgca ctgacctgct caagtttgcc gaaggcaata tctacgagga gcacccaaaag 1620
ttcatcaciaa cgtttgacga gaagtggcgc atggacgaga acataatcct gatcatgtgt 1680
gccattgtcc tttttacctc ggctcgatcg cgagtgatac acaaagacgt gattagattg 1740
gaacagaatt cctactatta tcttctgcga agatatctgg agagtgttta ttctggctgt 1800
gaggcgagaa acgcgtttat caagctaatc caaaagattt cagatgtgga gcgtctgaac 1860
aagttcataa ttaatgtcta tttgaatgtt aacccatccc aggtggagcc cttgctgcgt 1920
gaaatattcg atttgaaaaa tcac 1944

<210> 15

<211> 648

<212> PRT

<213> D. melanogaster

<400> 15

Asn Ile Met Ser Glu Glu Asp Lys Leu Ile Lys Arg Arg Lys Ile Glu
1 5 10 15

Thr Asn Arg Ala Lys Arg Arg Leu Met Glu Asn Gly Thr Asp Ala Cys
20 25 30

Asp Ala Asp Gly Gly Glu Glu Arg Asp His Lys Ala Pro Ala Asp Ser
35 40 45

Ser	Ser	Ser	Asn	Leu	Asp	His	Tyr	Ser	Gly	Ser	Gln	Asp	Ser	Gln	Ser	
50						55					60					
Cys	Gly	Ser	Ala	Asp	Ser	Gly	Ala	Asn	Gly	Cys	Ser	Gly	Arg	Gln	Ala	
65					70					75					80	
Ser	Ser	Pro	Gly	Thr	Gln	Val	Asn	Pro	Leu	Gln	Met	Thr	Ala	Glu	Lys	
				85					90					95		
Ile	Val	Asp	Gln	Ile	Val	Ser	Asp	Pro	Asp	Arg	Ala	Ser	Gln	Ala	Ile	
			100					105					110			
Asn	Arg	Leu	Met	Arg	Thr	Gln	Lys	Glu	Ala	Ile	Ser	Val	Met	Glu	Lys	
		115					120					125				
Val	Ile	Ser	Ser	Gln	Lys	Asp	Ala	Leu	Arg	Leu	Val	Ser	His	Leu	Ile	
	130					135					140					
Asp	Tyr	Pro	Gly	Asp	Ala	Leu	Lys	Ile	Ile	Ser	Lys	Phe	Met	Asn	Ser	
145					150					155					160	
Pro	Phe	Asn	Ala	Leu	Thr	Val	Phe	Thr	Lys	Phe	Met	Ser	Ser	Pro	Thr	
				165					170						175	
Asp	Gly	Val	Glu	Ile	Ile	Ser	Lys	Ile	Val	Asp	Ser	Pro	Ala	Asp	Val	
			180					185					190			
Val	Glu	Phe	Met	Gln	Asn	Leu	Met	His	Ser	Pro	Glu	Asp	Ala	Ile	Asp	
	195						200					205				
Ile	Met	Asn	Lys	Phe	Met	Asn	Thr	Pro	Ala	Glu	Ala	Leu	Arg	Ile	Leu	
	210					215						220				
Asn	Arg	Ile	Leu	Ser	Gly	Gly	Gly	Ala	Asn	Ala	Ala	Gln	Gln	Thr	Ala	
225					230					235					240	
Asp	Arg	Lys	Pro	Leu	Leu	Asp	Lys	Glu	Pro	Ala	Val	Lys	Pro	Ala	Ala	
				245					250					255		
Pro	Ala	Glu	Arg	Ala	Asp	Thr	Val	Ile	Gln	Ser	Met	Leu	Gly	Asn	Ser	
			260					265					270			

Pro Pro Ile Ser Pro His Asp Ala Ala Val Asp Leu Gln Tyr His Ser
275 280 285

Pro Gly Val Gly Glu Gln Pro Ser Thr Ser Ser Ser His Pro Leu Pro
290 295 300

Tyr Ile Ala Asn Ser Pro Asp Phe Asp Leu Lys Thr Phe Met Gln Thr
305 310 315 320

Asn Tyr Asn Asp Glu Pro Ser Leu Asp Ser Asp Phe Ser Ile Asn Ser
325 330 335

Ile Glu Ser Val Leu Ser Glu Val Ile Arg Ile Glu Tyr Gln Ala Phe
340 345 350

Asn Ser Ile Gln Gln Ala Ala Ser Arg Val Lys Glu Glu Met Ser Tyr
355 360 365

Gly Thr Gln Ser Thr Tyr Gly Gly Cys Asn Ser Ala Ala Asn Asn Ser
370 375 380

Gln Pro His Leu Gln Gln Pro Ile Cys Ala Pro Ser Thr Gln Gln Leu
385 390 395 400

Asp Arg Glu Leu Asn Glu Ala Glu Gln Met Lys Leu Arg Glu Leu Arg
405 410 415

Leu Ala Ser Glu Ala Leu Tyr Asp Pro Val Asp Glu Asp Leu Ser Ala
420 425 430

Leu Met Met Gly Asp Asp Arg Ile Lys Pro Asp Asp Thr Arg His Asn
435 440 445

Pro Lys Leu Leu Gln Leu Ile Asn Leu Thr Ala Val Ala Ile Lys Arg
450 455 460

Leu Ile Lys Met Ala Lys Lys Ile Thr Ala Phe Arg Asp Met Cys Gln
465 470 475 480

Glu Asp Gln Val Ala Leu Leu Lys Gly Gly Cys Thr Glu Met Met Ile
485 490 495

Met Arg Ser Val Met Ile Tyr Asp Asp Asp Arg Ala Ala Trp Lys Val

500

505

510

Pro His Thr Lys Glu Asn Met Gly Asn Ile Arg Thr Asp Leu L